

Db	62	YQ--	MEHDEHQNVQQLIGKTHEKQNV	PVLLDGRKALAA	MDRDLLELVDFFA	ILE	118																																													
QY	125	DTPEFAVRLIREAKAYLDL	PPPEFKALTHYAADGSY	MHC	PGHSGGVAFLKSPVGMF		184																																													
Db	119	DTADFLAGRAVAMTRYQO	LLPPLFSA	LMKYS	SDIHEXSWA	APHGQGVGT	KTIPARFY 178																																													
QY	185	HOFFGEMLRADVCNA	VDLGGLLDHTG	VAA	SERNARITNC	DLHYTN	GTSNKTIV 244																																													
Db	179	HDYVGERLFTPDW	IGERTIS	IGSLDHTG	AFGESEKTA	ARVPAD	RSWVVGTS	GSNRTI 238																																												
QY	245	MNSTVA	AGDLYVVD	RNCHKS	SVLHSLIM	TGAVV	VFPLMP	PRNHGII	IGPIPKSE	FAMENIOK 304																																										
Db	239	MOAMTDNDV	VVVD	RNCHKS	IEG	GLMTL	TAKK	LYVTV	PSRNK	YIGIIP	YPOEM	PETLOK 298																																								
QY	305	KIARNP	FATDK-NAK	PRVLLT	TOSTY	DVLYN	VEIKEM	LDGKID	ITLH	FDE	AMLPHATF 363																																									
Db	299	KISSP	LTCKKAGQ	PSYCV	VTTC	DGVCY	NAKE	ADL	EKTS	DRLH	FDE	AMVYARFN 358																																								
QY	364	DFG	DIYHAI	GAID	PRCKES	MVES	TOSTH	KLLAGLS	QAS	QILV	QAD	DQR	LD	RVFN	AYL 423																																					
Db	359	PIYADH	AMKGE	PGD	HNGP	VFAT	HTH	KLLNAL	SO	ASYI	HVR	EG-RGA	IN	SFR	QAYM 417																																					
QY	424	MHTST	QVYSII	ASC	VAA	AME	PGST	LV	YES	KEAL	D	PR	AR	K	YD	EE	MGTD--MMF 481																																			
Db	418	MHAT	STPL	VAIC	ASND	VA	SM	QNS	GLST	IG	CV	IDE	AV	D	E	FO	MA	RLYK	FAAD	SNFF 477																																
QY	482	KVW-----	-----	GP	T	D	S	E	D	G	L	E	R	D	A	M	L	K	A	N	E	R	M	G	F	N	L	D	523																							
Db	478	KPMNK	KEV	V	T	P	O	T	K	Y	T	P	A	D	A	T	K	L	L	---	T	Y	Q	D	C	W	V	N	H	P	E	S	N	H	G	F	D	I	P	D	M	S	M	L	D	534						
QY	524	IKAT	IT	P	R	D	L	V	E	G	S	D	E	F	G	I	P	A	I	V	T	K	L	E	N	G	Y	E	K	T	G	L	Y	S	F	F	M	T	I	G	I	T	K	R	N	58						
Db	535	IKV	SI	L	A	P	G	M	G	E	G	E	L	-E	E	T	G	V	P	A	L	V	T	A	M	L	G	R	H	G	I	V	P	R	T	T	D	F	O	I	M	E	L	F	S	M	G	T	R	G	M	593
QY	584	TMVA	L	O	O	F	P	D	D	V	D	K	O	L	M	K	V	L	E	R	V	O	K	N	P	-R	Y	E	R	V	G	K	D	L	C	T	O	I	H	E	V	Y	K	A	N	D	A	R	L	T	642	
Db	594	TLV	N	T	L	C	S	F	R	A	H	D	A	N	T	P	L	A	Q	V	N	E	L	V	E	O	P	D	T	Y	A	N	G	I	H	D	G	T	M	F	A	M	K	E	N	P	G	A	R	L	N	653
QY	643	EMY	L	S	D	V	P	A	M	K	P	T	D	A	S	K	A	N	K	I	E	R	V	A	I	D	L	E	G	R	V	T	A	L	L	P	P	P	G	I	P	L	L	I	G	E	R	-	700			
Db	654	EAS	G	L	F	V	A	L	I	T	R	E	A	N	A	L	V	D	N	N	E	L	V	E	I	S	N	L	P	G	I	A	N	S	I	P	P	R	P	G	I	P	M	L	S	E	N	G	D	711		
QY	701	NKV	I	V	N	Y	L	K	F	A	B	E	N	E	K	P	F	G	E	T	D	N	H	L	V	K	O	I	D	G	K	A	V	Y	V	D	C	Y	745													
Db	714	KN	S	P	O	V	S	Y	L	R	S	L	O	S	W	D	H	F	P	F	E	H	E	T	E	G	--T	E	I	I	D	G	--I	Y	H	M	C	V	K	755												

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RA Battra F.R.;
RA Butland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
RT "Analysis of the Escherichia coli genome VI: DNA sequence of the
RT region from 92.8 through 100 minutes."
RL Nucleic Acids Res. 23:2105-2119(1995).
RN [3]
RP SEQUENCE OF 1-78 FROM N.A.
RX MEDLINE=88137961; PubMed=2830169; DOI=10.1016/0378-1119(87)90333-7;
RA Webster C., Kempseil K., Booth I., Busby S.,
RT "Organisation of the regulatory region of the Escherichia coli
RL melibiose operon."
RL Gene 59:253-263(1987).
RN [4]
RP SEQUENCE OF 1-7.
RX MEDLINE=74086944; PubMed=4204273;
RA Sabo D.L., Fischer E.H.;
RT "Chemical properties of Escherichia coli lysine decarboxylase
RL including a segment of its pyridoxal 5'-phosphate binding site."
RL Biochemistry 13:670-676(1974).
CC -1- FUNCTION: ADC can be found in two forms: biodegradative and
CC biosynthetic. The biodegradative form may play a role in
CC regulating pH by consuming proteins.
CC -1- CATALYTIC ACTIVITY: L-arginine = agmatine + CO(2).
CC -1- COFACTOR: Pyridoxal phosphate.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- INDUCTION: Under conditions of acidic pH, anaerobiosis and rich
CC medium.
CC -1- SIMILARITY: Belongs to the Orn/Lys/Arg decarboxylase class-I
CC family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/announce/
CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL, M93362; AAA23481.1; -.
CC EMBL, U14003; AAA97017.1; ALT INIT.
CC EMBL, U00006; AAC77078.1; ALT INIT.
CC EMBL, M18425; -; NOT_ANNOTATED_CDS.
CC PIR, S56346; S56346.
CC HSSP, P43099; IC4K.
CC ECHOBASE; EBI464; -.
CC Ecogene; EGI1501; adA.
CC InterPro: IPR011006; CheY like.
CC InterPro: IPR000310; Decarboxylase.
CC InterPro: IPR008286; Decarboxylase_C.
CC InterPro: IPR005308; ORN_DC_1_N.
CC InterPro: IPR011193; Orn_decarb.
CC Pfam; PF01276; ORN_DC_1; 1.
CC Pfam; PF03711; ORN_DC_1_C; 1.
CC Pfam; PF03709; ORN_DC_1_N; 1.
CC PIRSF, PIRSF009393; Orn_decarb; 1.
CC PROSITE; PS00703; ORN_DC_1; 1.
CC Complete proteome; Decarboxylase; Direct protein sequencing; Lyase;
KM Pyridoxal phosphate.
FT BINDING 386 Pyridoxal phosphate.
FT CONFLICT 75 L->P (in Ref. 3).
FT SEQUENCE 755 AA; 84425 MW; 0FCB71514649F8F CRC64;
SQ
Query Match 34.9%; Score 1378.5; DB 1; Length 755;
Best Local Similarity 37.1%; Pred. No. 7.8e-87;
Matches 284; Conservative 157; Mismatches 284; Indels 41; Gaps 14.

7 IVIIDEDPRSENS-SGLGIRVLAAIEDEGLVGVGYSGYGLTFSFAQOQSASAFILSID 65
:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 3 VLIVSESELDHDTGWAGNAVERLADLSQONTVTKSTFSFD--GFALLSSNEAIDCLMFS 60
:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
66 DELIVEEKPAIEQLRNPFVORIRNRNEIPIFLGGE--TRTSRHLPNDVLRFLHGFIHNNE 124
:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

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Db      61 YQ---MEHPDEHQNVROLIGKHERQONVPVFLGLDREKLAAMDRLLELVEDEFAMILE 117
Qy      125 DTPEFVARLIIREKAKYLDLSPPEFKALTHYAADGSYSMHCPGSGVAFLKSPYQOMF 184
Db      118 DTDDEFIAGRAVAAATRYRQQLPPLFSALMKYSIDHEYSNAPRHOGSGVGTFTKTPAGRGY 177
Qy      185 HOFEGENMLRADVCNAVDLQGLDHTGTPVAASERNARATYNCDELTVFNTGTSNKTIV 244
Db      178 HDVYGENLFRTDMGIERSTLSGLDHTGAFGESEKAAAFVGAADRSMSVVGTSNRTI 237
Qy      245 WNSTVAPGDIYVDRNCHSVLHISIMTGAVPVFLMPTNHHGIIIGPIKSEFAMENIOK 304
Db      238 MQACMTNDVVVDRNCHSIEOGMLTGAKPVYVWPSNRKGIIGPIYQEQMPELTOK 297
Qy      305 KIARNPATDK-NAKPRVLTITOSTYDGVLYNVEIEKMLDGKIDTLHFDEAMLPATPH 363
Db      298 KISSPLTKDAGOKPSYCVVNTCTYDGCYNAAEADLEKTSDBRLHFBAMYGARFN 357
Qy      364 DFYGDYHAIAGDRPRCKESMVFSTOSTHKLALGSLQASOILVODADQNRDLDRVFEAYL 423
Db      358 PIYADHYARNGEPDNGPTVFATHSTHKLNALSQASYIHVREG-RGAINFSRFQAYM 416
Qy      424 MHTSTPOYSIIASCDAVAAAMEAPGCTALVEESLKEALDPRFARKVDEMGTD--WMP 481
Db      417 MHATTSPLYAICASNDVAVSMNDGNSGLTQEVIDEAVDFRQAMARLYKEFTADGSMWF 476
Qy      482 KVM-----GPTDLSBDGLEBRDAMMLKANERHMGFNGMLAEGFNNLDP 523
Db      477 KPMKEVVTDPQGTGYDFAADAPTKL---TTVQDCVWVHGPESMNGFKDIPDNMSGLDP 533
Qy      524 IKATITTPGLDVEGDFSDFGIPALVITYKLAHGVIVETGLYSFFIMFTIGITKGRN 583
Db      534 IKVSIILAPMGEGDEL-EETGVPAALVTAMIGRGIVPRTTDFQIMFLFSMGVTRGKMG 592
Qy      584 TMYAALQOFKDDYDKQPLMKVLPFVQKHP-RYEVNGKDLCTQJHEHYKANDVALLTT 642
Db      593 TLVNTLCSFKHYANPPLAOWMPELVEQPYTYANNGIHDLGDTMAMLEKNNPGARLN 652
Qy      643 EMTYSDMWPAKPTDAFSKMAHRIERYAIDLEGRAVAVLLTPYPGIPLLIPGERF-- 700
Db      653 EAYSGLPVAEITPREAYNAIVDNNVELVISIENLPRIANSVIYPPGIPMLLSGENFGD 712
Qy      701 -NKVIYNYLKFAREFNEKFPGETDNHGLVKQIVDGAAYVYDVCYK 745
Db      713 KNSPOVSYLRSLSQMDHFFPGFEHETEG--TEIIDG--IYHWVCVK 754

RESULT 13
ID      06XJ52 PRELIMINARY; PRT; 756 AA.
AC      06XJ52;
DT      05-JUL-2004 (TREMblrel. 27, Created)
DT      05-JUL-2004 (TREMblrel. 27, Last sequence update)
DE      05-JUL-2004 (TREMblrel. 27, Last annotation update)
DE      Arginine decarboxylase.
GN      Name=adi;
OS      Shigella boydii.
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC      Enterobacteriaceae; Shigella.
CX      NCBI_TaxID=621;
RN      (1)
RP      SEQUENCE FROM N.A.
RC      STRAIN=CDPH;
RA      Chan Y.C., Blaschek H.P.;
RL      Submitted (FEB-2003) to the EMBL/Genbank/DBJ databases.
DR      EMBL, AY231474; AAF59882.1;
DR      GO:GO:0005737; C:cytoplasm; IEA.
DR      GO:GO:0016831; F:carboxy-lyase activity; IEA.
DR      GO:GO:0003824; F:catalytic activity; IEA.
DR      GO:GO:0006520; P:amino acid metabolism; IEA.
DR      InterPro: IPR01006; CheY like.
DR      InterPro: IPR000310; Decarboxylase.
DR      InterPro: IPR008286; Decarboxylase_C.

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DR      InterPro: IPR005308; OKR_DC_1_N.
DR      InterPro: IPR011193; Orn_decarb.
DR      Pfam: PF01276; OKR_DC_1_1.
DR      Pfam: PF03711; OKR_DC_1_C_1.
DR      Pfam: PF03709; OKR_DC_1_N_1.
DR      Pfam: PF03709; OKR_DC_1_N_1.
DR      FIRST, FIRST00393; Orn_decarb; 1.
DR      PROSITE, PS00703; OKR_DC_1_1.
SQ      SEQUENCE 756 AA; 84690 MW; C26B2B3B3CAA71F CRC64;

Query Match      34.8%; Score 1377.5; DB 2; Length 756;
Best Local Similarity 37.1%; Pred No. 9.2e-87;
Matches 284; Conservative 157; Mismatches 284; Indels 41; Gaps 14;

Qy      7 IVIDEDPSENS-SGLGIRYLAKEIEDEGLVLTGYSYGLDYSFAQOGRSAPFLSLID 65
Db      4 VLIYSEFLHDTQWGNAYERLADLSQONVTVIKSTFDD--GFAILSNBAIDCLMPS 61
Qy      66 DEEIVEKEEALIQLNFOEIRYNEEIPITLHGE-TYTSNHIENDVARELHGFIHME 124
Db      62 YQ---MEHPDEHQNVROLIGKHERQONVPVFLDDEKALAMORDLLELVEDEFAMILE 118
Qy      125 DTPEFVARLIIREKAKYLDLSPPEFKALTHYAADGSYSMHCPGSGVAFLKSPYQOMF 184
Db      119 DTDDEFIAGRAVAAATRYRQQLPPLFSALMKYSIDHEYSNAPRHOGSGVGTFTKTPAGRGY 178
Qy      185 HOFEGENMLRADVCNAVDLQGLDHTGTPVAASERNARATYNCDELTVFNTGTSNKTIV 244
Db      179 HDVYGENLFRTDMGIERSTLSGLDHTGAFGESEKAAAFVGAADRSMSVVGTSNRTI 238
Qy      245 WNSTVAPGDIYVDRNCHSVLHISIMTGAVPVFLMPTNHHGIIIGPIKSEFAMENIOK 304
Db      239 MQACMTNDVVVDRNCHSIEOGMLTGAKPVYVWPSNRKGIIGPIYQEQMPELTOK 298
Qy      305 KIARNPATDK-NAKPRVLTITOSTYDGVLYNVEIEKMLDGKIDTLHFDEAMLPATPH 363
Db      299 KISESLTKDAGOKPSYCVVNTCTYDGCYNAAEADLEKTSDBRLHFBAMYGARFN 358
Qy      364 DFYGDYHAIAGDRPRCKESMVFSTOSTHKLALGSLQASOILVODADQNRDLDRVFEAYL 423
Db      359 PIYADHYARNGEPDNGPTVFATHSTHKLNALSQASYIHVREG-RGAINFSRFQAYM 417
Qy      424 MHTSTPOYSIIASCDAVAAAMEAPGCTALVEESLKEALDPRFARKVDEMGTD--WMP 481
Db      418 MHATTSPLYAICASNDVAVSMNDGNSGLTQEVIDEAVDFRQAMARLYKEFTADGSMWF 477
Qy      482 KVM-----GPTDLSBDGLEBRDAMMLKANERHMGFNGMLAEGFNNLDP 523
Db      478 KPMKEVVTDPQGTGYDFAADAPTKL---TTVQDCVWVHGPESMNGFKDIPDNMSGLDP 534
Qy      524 IKATITTPGLDVEGDFSDFGIPALVITYKLAHGVIVETGLYSFFIMFTIGITKGRN 583
Db      535 IKVSIILAPMGEGDEL-EETGVPAALVTAMIGRGIVPRTTDFQIMFLFSMGVTRGKMG 593
Qy      584 TMYAALQOFKDDYDKQPLMKVLPFVQKHP-RYEVNGKDLCTQJHEHYKANDVALLTT 642
Db      594 TLVNTLCSFKHYANPPLAOWMPELVEQPYTYANNGIHDLGDTMAMLEKNNPGARLN 653
Qy      643 EMTYSDMWPAKPTDAFSKMAHRIERYAIDLEGRAVAVLLTPYPGIPLLIPGERF-- 700
Db      654 EAYSGLPVAEITPREAYNAIVDNNVELVISIENLPRIANSVIYPPGIPMLLSGENFGD 713
Qy      701 -NKVIYNYLKFAREFNEKFPGETDNHGLVKQIVDGAAYVYDVCYK 745
Db      714 KNSPOVSYLRSLSQMDHFFPGFEHETEG--TEIIDG--IYHWVCVK 755

RESULT 14
ID      08Z1P1 PRELIMINARY; PRT; 756 AA.
AC      08Z1P1; 07C5L6;
DT      01-MAR-2002 (TREMblrel. 20, Created)
DT      01-MAR-2002 (TREMblrel. 20, Last sequence update)
DT      25-OCT-2004 (TREMblrel. 28, Last annotation update)

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